

ATGAGAAGGTGTAGAATAAGTGGGAGGCCCCCGGCGCCCCCGGTGTCCCCGCCAGGCC
 MetArgArgCysArgIleSerGlyArgProProAlaProProGlyValProAlaGlnAla
 CCTGTCTCCCAGCCTGATGCCCTGGCCACCAGAGGAAAGTGGTGTTCATGGATAGATGTG
 ProValSerGlnProAspAlaProGlyHisGlnArgLysValValSerTrpIleAspVal
 TATACTCGCGCTACCTGCCAGCCCCGGGAGGTGGTGGTGGCCCTTGACTGTGGAGCTCATG
 TyrThrArgAlaThrCysGlnProArgGluValValValProLeuThrValGluLeuMet
 GGCACCGTGGCCAAACAGCTGGTGGCCAGCTGCGTGAAGTGTGCAGCGCTGTGGTGGCTGC
 GlyThrValAlaLysGlnLeuValProSerCysValThrValGlnArgCysGlyGlyCys
 TGCCCTGACGATGGCCTGGAGTGTGTGCCCACTGGGCAGCACCAAGTCCGGATGCAGATC
 CysProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMetGlnIle
 CTCATGATCCGGTACCCGAGCAGTCAGCTGGGGGAGATGTCCCTGGAAGAACACAGCCAG
 LeuMetIleArgTyrProSerSerGlnLeuGlyGluMetSerLeuGluGluHisSerGln
 TGTGAATGCAGACCTAAAAAAGGACAGTGTGTGAAGCCAGACAGGGCTGCTACTCCC
 CysGluCysArgProLysLysLysAspSerAlaValLysProAspArgAlaAlaThrPro
 CACCACCGTCCCCAGCCCCGTTCTGTTCGGGGCTGGGACTCTGCCCCCGGAGCACCCCTCC
 HisHisArgProGlnProArgSerValProGlyTrpAspSerAlaProGlyAlaProSer
 CCAGCTGACATACCCCAATCCCACTCCAGCCCCAGGCCCTCTGCCCACGCTGCACCCAG
 ProAlaAspIleThrGlnSerHisSerSerProArgProLeuCysProArgCysThrGln
 CACCACCAGTGCCCTGACCCCCGGACCTGCCGCTGCCGCTGTGACGCGCGAGCTTCCTC
 HisHisGlnCysProAspProArgThrCysArgCysArgCysArgArgSerPheLeu
 CGTTGTCAAGGGCGGGCTTAGAGCTCAACCCAGACACCTGCAGGTGCCGGAAGCTGCGA
 ArgCysGlnGlyArgGlyLeuGluLeuAsnProAspThrCysArgCysArgLysLeuArg
 AGGTGA
 ArgEnd

FIGURE

1

1/1

09033662.030399

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      10      20      30      40      50
MNFLLSVHWSLALLLYLHAKWSQAAPMAEGGQNH-EVVKFMDVYQRSYC
      ::||::: ::::|: ||:::| | | |
MRRCRISGRPPAPPGVPAQAPVSPDAPGHQRKVSVSWIDVYTRATC

      60      70      80      90     100     110
HPIETLVDFIQEYPDEIEYIFKPCVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPH
:| |::| : | :::: : |||:: ||||| :|||::|::: : : ||::|: :
QPREVVVPLTVELMGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIR-Y

      120     130           140     150     160
QGQHIGEMSFLQHNKCECRPKK-----DRA-----RQEKKSVRGKGGQKRKRKKSRY
: : |||: : |||::| | | | | | | | | | | | | | | | | | | | | | | |
PSSQLGEMSLSEHSQCECRPKKKDSAVKPDRAATPHHRPQPRSVPGWDSAPGAPSPADIT

      170     180     190     200     210
KWSVPCGPCSERRKHLFVQDPQTCKCCKNTD-SRCKARQLELNERTCRCDKPRR
: | | | | : | : |||::|::: : ||::| ||| | ||| | | |
QSHSSPRPLCPRCTQHHQCPDPRTCRCRCRRRSFLRCQGRGLELNPDTCRCRKLRR

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Figure 2. Sequence alignment of VEGF3(lower line) compared to VEGF from human (upper line).

FIGURE 2 1/1

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